CRF Errors Corrected by the STIC Systems Branch

ENTERED

Serial Number: 09/856,681

CRF Processing Date: 10/16/2001
Edited by: _____
Verified by: _____ (STIC staf

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was wrapped down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patentin bug). Sequences corrected: _____

☑ Other: Seq 2 - corrected amino acid nos.
_____
_____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/856,681

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\10162001\I856681.raw

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 3 <110> APPLICANT: Behl, Christian
 4         Klostermann, Andreas
 6 <120> TITLE OF INVENTION: Human semaphorin 6A-1 (SEMA6A-A), a gene involved
 7         in neuronal development and regeneration mechanisms
 8         during apoptosis, and its use as a potential drug target
10 <130> FILE REFERENCE: 48498-258443
12 <140> CURRENT APPLICATION NUMBER: 09/856,681
13 <141> CURRENT FILING DATE: 2001-05-22
15 <150> PRIOR APPLICATION NUMBER: PCT/EP99/09215
16 <151> PRIOR FILING DATE: 1999-11-26
18 <150> PRIOR APPLICATION NUMBER: 98122441.3
19 <151> PRIOR FILING DATE: 1998-11-26
21 <160> NUMBER OF SEQ ID NOS: 7
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 3093
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
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32 <222> LOCATION: (1)..(3093)
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43 aac tat aca aaa cag tat ccg gtg ttt gtg ggc cac aag cca gga cgg   144
44 Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
45          35                  40                  45
47 aac acc aca cag agg cac agg ctg gac atc cag atg att atg atc atg   192
48 Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
49      50                  55                  60
51 aac gga acc ctc tac att gct gct agg gac cat att tat act gtt gat   240
52 Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
53  65                  70                  75                  80
55 ata gac aca tca cac acg gaa gaa att tat tgt agc aaa aaa ctg aca   288
56 Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
57                  85                  90                  95
60 tgg aaa tct aga cag gcc gat gta gac aca tgc aga atg aag gga aaa   336
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62             100                 105                 110
64 cat aag gat gag tgc cac aac ttt att aaa gtt ctt cta aag aaa aac   384
65 His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
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68 gat gat gca ttg ttt gtc tgt gga act aat gcc ttc aac cct tcc tgc   432
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 72 aga aac tat aag atg gat aca ttg gaa cca ttc ggg gat gaa ttc agc      480
 73 Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
 74 145                 150                 155                 160
 76 gga atg gcc aga tgc cca tat gat gcc aaa cat gcc aac gtt gca ctg      528
 77 Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
 78                 165                 170                 175
 80 ttt gca gat gga aaa cta tac tca gcc aca gtg act gac ttc ctt gcc      576
 81 Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
 82                 180                 185                 190
 84 att gac gca gtc att tac cgg agt ctt gga gaa agc cct acc ctg cgg      624
 85 Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
 86                 195                 200                 205
 88 acc gtc aag cac gat tca aaa tgg ttg aaa gaa cca tac ttt gtt caa      672
 89 Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
 90     210                 215                 220
 92 gcc gtg gat tac gga gat tat atc tac ttc ttc ttc agg gaa ata gca      720
 93 Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala
 94 225                 230                 235                 240
 96 gtg gag tat aac acc atg gga aag gta gtt ttc cca aga gtg gct cag      768
 97 Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
 98                 245                 250                 255
100 gtt tgt aag aat gat atg gga gga tct caa aga gtc ctg gag aaa cag      816
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102                 260                 265                 270
104 tgg acg tcg ttc ctg aag gcg cgc ttg aac tgc tca gtt cct gga gac      864
105 Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
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108 tct cat ttt tat ttc aac att ctc cag gca gtt aca gat gtg att cgt      912
109 Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
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113 Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
114 305                 310                 315                 320
116 agc atc cct ggg tct gca gtc tgt gcc tat gac atg ctt gac att gcc     1008
117 Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
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120 agt gtt ttt act ggg aga ttc aag gaa cag aag tct cct gat tcc acc     1056
121 Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
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125 Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
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128 tgt gct ggc tca tcc tcc tta gaa aga tat gca acc tcc aat gag ttc     1152
129 Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
130     370                 375                 380
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138                     405                 410                 415
140 aga tac cgc ctt acc aaa att gca gtg gac aca gct gct ggg cca tat   1296
141 Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
142                 420                 425                 430
144 cag aat cac act gtg gtt ttt ctg gga tca gag aag gga atc atc ttg   1344
145 Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
146             435                 440                 445
148 aag ttt ttg gcc aga ata gga aat agt ggt ttt cta aat gac agc ctt   1392
149 Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
150     450                 455                 460
152 ttc ctg gag gag atg agt gtt tac aac tct gaa aaa tgc agc tat gat   1440
153 Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
154 465                 470                 475                 480
156 gga gtc gaa gac aaa agg atc atg ggc atg cag ctg gac aga gca agc   1488
157 Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
158                 485                 490                 495
160 agc tct ctg tat gtt gcg ttc tct acc tgt gtg ata aag gtt ccc ctt   1536
161 Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
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164 ggc cgg tgt gaa cga cat ggg aag tgt aaa aaa acc tgt att gcc tcc   1584
165 Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
166         515                 520                 525
168 aga gac cca tat tgt gga tgg ata aag gaa ggt ggt gcc tgc agc cat   1632
169 Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
170     530                 535                 540
172 tta tca ccc aac agc aga ctg act ttt gag cag gac ata gag cgt ggc   1680
173 Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
174 545                 550                 555                 560
177 aat aca gat ggt ctg ggg gac tgt cac aat tcc ttt gtg gca ctg aat   1728
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182 Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
183             580                 585                 590
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186 Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
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190 Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
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193 cat aat cac caa gac aag aag gga gtg att cgg gaa agt tac ctc aaa   1920
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195 625                 630                 635                 640
197 ggc cac gac cag ctg gtt ccc gtc acc ctc ttg gcc att gca gtc atc   1968
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205 gtc tgt gat cat cgg cgc aaa gac gtg gct gtg gtg cag cgc aag gag    2064
206 Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu
207         675             680             685
209 aag gag ctc acc cac tcg cgc cgg ggc tcc atg agc agc gtc acc aag    2112
210 Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
211     690             695             700
213 ctc agc ggc ctc ttt ggg gac act caa tcc aaa gac cca aag ccg gag    2160
214 Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
215 705             710             715             720
217 gcc atc ctc acg cca ctc atg cac aac ggc aag ctc gcc act ccc ggc    2208
218 Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
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221 aac acg gcc aag atg ctc att aaa gca gac cag cac cac ctg gac ctg    2256
222 Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
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225 acg gcc ctc ccc acc cca gag tca acc cca acg ctg cag cag aag cgg    2304
226 Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg
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229 aag ccc agc cgc ggc agc cgc gag tgg gag agg aac cag aac ctc atc    2352
230 Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
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233 aat gcc tgc aca aag gac atg ccc ccc atg ggc tcc cct gtg att ccc    2400
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237 acg gac ctg ccc ctg cgg gcc tcc ccc agc cac atc ccc agc gtg gtg    2448
238 Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
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241 gtc ctg ccc atc acg cag cag ggc tac cag cat gag tac gtg gac cag    2496
242 Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
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245 ccc aaa atg agc gag gtg gcc cag atg gcg ctg gag gac cag gcc gcc    2544
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247         835             840             845
249 aca ctg gag tat aag acc atc aag gaa cat ctc agc agc aag agt ccc    2592
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261 cag acc ggt cta agc aag cgg ctg gaa atg cac cac tcc tct tcc tac    2736
262 Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr
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266 Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser
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270 His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser
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273 tct cac ctc tcc aga aac cag agc ttt ggc agg gga gac aac ccg ccg   2880
274 Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
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277 ccc gcc ccg cag agg gtg gac tcc atc cag gtg cac agc tcc cag cca   2928
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282 Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
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312         35              40              45
314 Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
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317 Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
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323 Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/856,681

DATE: 10/16/2001
TIME: 18:00:23

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Output Set: **N:\CRF3\10162001\I856681.raw**